

Fig 1. Examples of two test sets of peptides and results with PKC-theta

A. P+1 test set

Position P+1					
Symbolic Representation: ddddRdd-S-?dd					
	Peptide Sequence	CPM	Ratio to Mean	Log Score	
1	ddddRdd-S-D dd	67 ± 3	0.4	-1.26 ± 0.03	
2	ddddRdd-S-N dd	88 ± 3	0.5	-0.87 ± 0.04	
3	ddddRdd-S-Q dd	158 ± 4	1.0	-0.03 ± 0.04	
4	ddddRdd-S-R dd	177 ± 9	1.8	0.00 ± 0.04	
5	ddddRdd-S-K dd	161 ± 18	1.6	0.00 ± 0.08	
6	ddddRdd-S-H dd	163 ± 10	1.0	0.01 ± 0.09	
7	ddddRdd-S-S dd	136 ± 3	0.8	-0.24 ± 0.03	
8	ddddRdd-S- dd	90 ± 3	0.6	-0.86 ± 0.07	
9	ddddRdd-S-L dd	239 ± 18	1.9	0.89 ± 0.11	
10	ddddRdd-S-F dd	164 ± 8	1.9	1.62 ± 0.03	
11	ddddRdd-S-W dd	135 ± 6	0.8	-0.25 ± 0.07	
12	ddddRdd-S-G dd	93 ± 2	0.6	-0.79 ± 0.03	
13	ddddRdd-S-A dd	97 ± 5	0.6	-0.73 ± 0.10	

B. P+2 test set

Position P+2					
Symbolic Representation: ddddRdd-S-F?d					
	Peptide Sequence	CPM	Ratio to Mean	Log Score	
1	ddddRdd-S-F D d	186 ± 11	0.5	-1.12 ± 0.08	
2	ddddRdd-S-F N d	188 ± 22	0.5	0.00 ± 0.04	
3	ddddRdd-S-F Q d	229 ± 7	0.6	-0.83 ± 0.05	
4	ddddRdd-S-F R d	228 ± 38	0.5	0.00 ± 0.05	
5	ddddRdd-S-F K d	200 ± 25	0.5	0.00 ± 0.05	
6	ddddRdd-S-F H d	238 ± 35	0.5	0.00 ± 0.06	
7	ddddRdd-S-F S d	431 ± 10	1.1	0.09 ± 0.05	
8	ddddRdd-S-F d	148 ± 3	0.4	-1.46 ± 0.03	
9	ddddRdd-S-F L d	489 ± 5	1.2	0.27 ± 0.01	
10	ddddRdd-S-F F d	543 ± 19	1.3	0.42 ± 0.07	
11	ddddRdd-S-F W d	459 ± 3	1.1	0.18 ± 0.01	
12	ddddRdd-S-F G d	195 ± 2	0.5	-1.05 ± 0.01	
13	ddddRdd-S-F A d	201 ± 7	0.5	-1.01 ± 0.07	

Fig 3: Raw Counts For In Vitro phosphorylation by PKC-theta
of a collection of peptides designed for analysis of PKC specific

Residue	-4	-3	-2	-1	P0	+1	+2	+3
D	277	178	419	294		67	186	263
N	422	153	477	651		88		610
Q	411	1	493	472		158	229	358
R								
K		117						
H	573	117		461		163		506
S	433	90	389	371	461	136	431	304
	439	93	458	376		30	148	226
L	640	85	347	413			489	715
F	741		243	348			543	647
W	721	151	301	290		135	459	470
G	517	127	449	672		93	195	409
A	380	83	362	678		97	201	711
T					402			
Geo Mean For Set	572	133	509	481	430	161	406	488

Fig 4: Ratio to Mean for PKC-theta

Residue	-4	-3	-2	-1	P0	+1	+2	+3
D	0.5	0.6	0.8	0.6		0.4	0.5	0.5
N	0.7	1.1	0.9	1.4		0.5		1.3
Q	0.7		1.0	1.0		1.0	0.6	0.7
R								
K		0.9						
H	1.0	0.9		1.0		1.0		1.0
S	0.8	0.7	0.8	0.8	1.1	0.8	1.1	0.6
	0.8	0.7	0.9	0.8		0.6	0.4	0.5
L	1.1	0.6	0.7	0.9			1.2	1.5
F	1.3		0.5	0.7			1.3	1.3
W	1.3	1.1	0.6	0.6		0.8	1.1	1.0
G	0.9	1.0	0.9	1.4		0.6	0.5	0.8
A	0.7	0.6	0.7	1.4		0.6	0.5	1.5
T					0.9			

Fig 6. A superset of degenerate peptides designed to extend analysis of PKC specificity

Supers t:		Superset A					
Anchor d Residues		Rxx-S-F					
Set		Set P-7	Set P-6	Set P-5	Set P-4	Set P-3	Set P-2
Position		P-7	P-6	P-5	P-4	P-3	P-2
Symbolic Representation of Set		ddd?Rdd-S-Fdd	dddR?d-S-Fdd	dddRdd-S-Fdd	dddRdd-S-F?dd	dddRdd-S-F?dd	dddRdd-S-F?dd
Residue within a variable position that vary	Other residues in class						
		D	E				
		9D999R99-S-F99	9D999R99-S-F99	99D99R99-S-F99	99R99-S-F99D99	99R99-S-F99D99	99R99-S-F999D
		9A999R99-S-F99	9A999R99-S-F99	99A99R99-S-F99	99R99-S-F99A99	99R99-S-F99A99	99R99-S-F999A
		9Q999R99-S-F99	9Q999R99-S-F99	99Q99R99-S-F99	99R99-S-F99Q99	99R99-S-F99Q99	99R99-S-F999Q
		9R999R99-S-F99	9R999R99-S-F99	99R99R99-S-F99	99R99-S-F99R99	99R99-S-F99R99	99R99-S-F999R
		9K999R99-S-F99	9K999R99-S-F99	99K99R99-S-F99	99R99-S-F99K99	99R99-S-F99K99	99R99-S-F999K
		9H999R99-S-F99	9H999R99-S-F99	99H99R99-S-F99	99R99-S-F99H99	99R99-S-F99H99	99R99-S-F999H
		9S999R99-S-F99	9S999R99-S-F99	99S99R99-S-F99	99R99-S-F99S99	99R99-S-F99S99	99R99-S-F999S
		9L999R99-S-F99	9L999R99-S-F99	99L99R99-S-F99	99R99-S-F99L99	99R99-S-F99L99	99R99-S-F999L
		9F999R99-S-F99	9F999R99-S-F99	99F99R99-S-F99	99R99-S-F99F99	99R99-S-F99F99	99R99-S-F999F
		9V999R99-S-F99	9V999R99-S-F99	99V99R99-S-F99	99R99-S-F99V99	99R99-S-F99V99	99R99-S-F999V
		9G999R99-S-F99	9G999R99-S-F99	99G99R99-S-F99	99R99-S-F99G99	99R99-S-F99G99	99R99-S-F999G
		9A999R99-S-F99	9A999R99-S-F99	99A99R99-S-F99	99R99-S-F99A99	99R99-S-F99A99	99R99-S-F999A

**Fig 7. Extension of Position-specific
scoring matrix for PKC-theta**

Residue	Experimentally determined										
	-7	-6	-5	+4	+5	+6					
D	0.9	-0.5	0.9	-0.3	-0.4	-0.4					
E											
N	0.1	-0.1	-0.2	-0.1		0.1					
Q	-0.2	0.0	-0.2	-0.2	0.0	-0.3					
R	0.3				0.0						
K	0.4				0.5						
H	-0.1	-0.1	0.1		0.2	0.0					
S	0.0	0.1	0.4	0.4	-0.2	0.1					
T											
	0.5	0.3	-0.2	0.0	0.0	0.1					
L	0.0	-0.5	0.5	-0.6	0.3	-0.3					
M											
F	0.0	-0.3	0.1	-0.3	-0.1	0.1					
Y											
W	-0.9	-0.4	-0.5	-0.8	-0.5	-1.1					
G	0.4	0.1	-0.2	0.0	0.0	0.1					
A	0.0	-0.2	-0.2	-0.3	-0.4	0.1					

Fig 8. Sequence Logo vs PSSM Logo

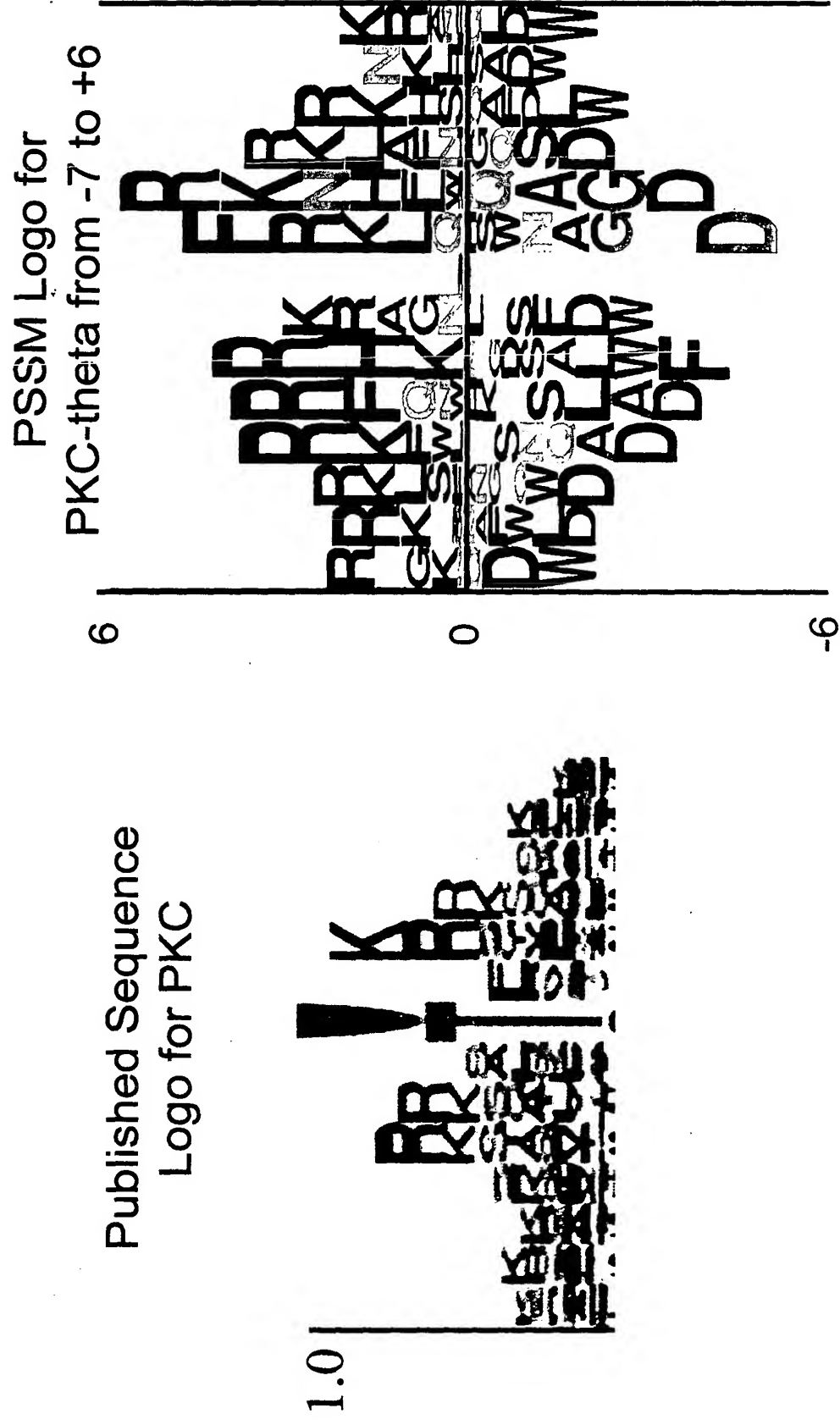


Fig 9. Testing our predictions for PKC- θ and Scansite prediction for PKC- δ against results for PKC- δ

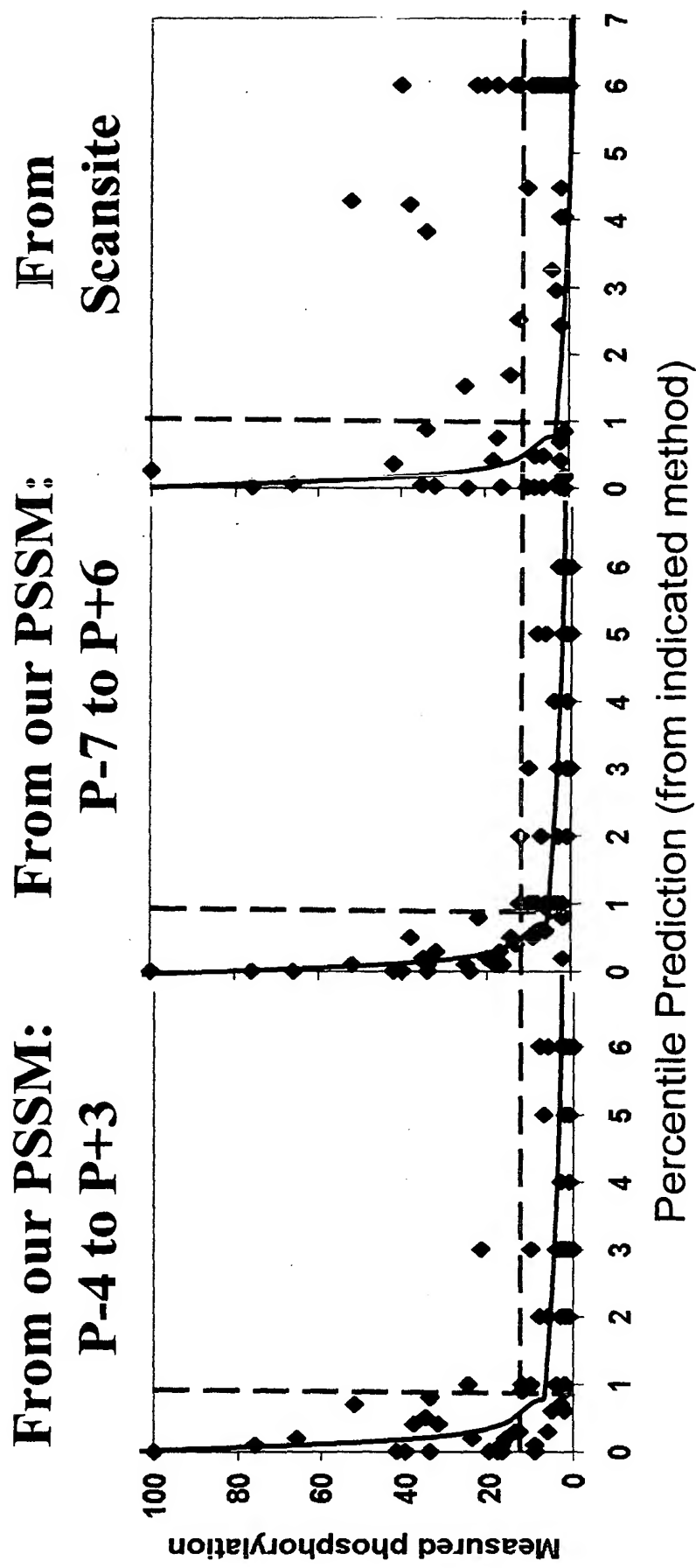


Fig 10: Comparison of our scoring with Scansite scoring for PKC-delta

Criteria:

Positive score: better than 1st percentile

Positive phosphorylation: better than 10% of max

Ours

	Measured activity	
	Positive	Negative
Prediction score	21	4
	2	48
Total Scored	75	
Sensitivity	92	
Specificity	91	

Scansite

	Measured activity	
	Positive	Negative
Prediction score	10	16
	12	37
Total Scored	75	
Sensitivity	70	
Specificity	45	

Fig 11. Prospective validation of scoring for PKC-theta PSM

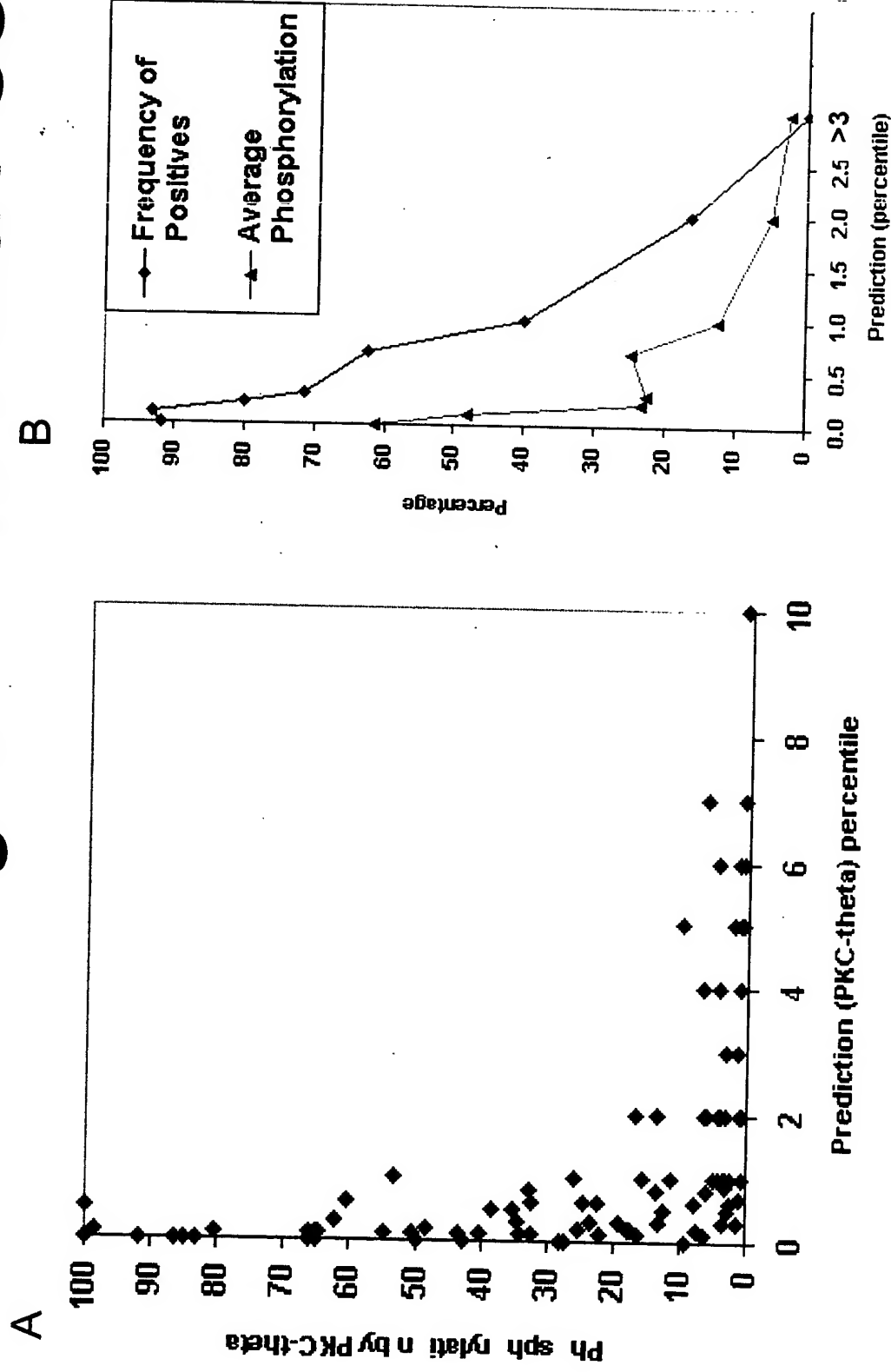


Fig 12. The d??R??S??d superset of test sets
with 1 anchor position

Symbolic Representation		d??R??-S-????d									
Anchor and phospho residues		Rxx-S									
Set		Set P-5	Set P-4	Set P-2	Set P-1	Set P+1	Set P-2	Set P+3	Set P+4		
P site n		P-5	P-4	P-2	P-1	P+1	P-2	P+3	P+4		
Symbolic Representation of Set		d?dRdd-S-ddddd	dd?Rdd-S-ddddd	dddR?d-S-ddddd	dddRd?-S-ddddd	dddRdd-S-?ddddd	dddRdd-S-d?ddddd	ddd?Rdd-S-dd?dd	ddd?Rdd-S-ddd?d		
Residues that vary within a variable position	Other residues										
	R	dRdRdd-S-ddddd	ddRRdd-S-ddddd	dddRRd-S-ddddd	dddRRd-S-ddddd	dddRRd-S-Rddddd	dddRdd-S-dRddddd	dddRdd-S-ddRdd	dddRdd-S-dddRdd	dddRdd-S-dddRdd	
	K	dKdRdd-S-ddddd	ddKRdd-S-ddddd	dddRKd-S-ddddd	dddRKd-S-ddddd	dddRKd-S-Kddddd	dddRdd-S-dKddddd	dddRdd-S-ddKdd	dddRdd-S-dddKdd	dddRdd-S-dddKdd	
	H	dHdRdd-S-ddddd	ddHRdd-S-ddddd	dddRHd-S-ddddd	dddRHd-S-ddddd	dddRHd-S-Hddddd	dddRdd-S-dHddddd	dddRdd-S-ddHdd	dddRdd-S-dddHdd	dddRdd-S-dddHdd	
	D	dDdRdd-S-ddddd	ddDRdd-S-ddddd	dddRDd-S-ddddd	dddRDd-S-ddddd	dddRDd-S-Dddddd	dddRdd-S-dDddddd	dddRdd-S-ddDdd	dddRdd-S-dddDdd	dddRdd-S-dddDdd	
	E	dEdRdd-S-ddddd	ddERdd-S-ddddd	dddREd-S-ddddd	dddREd-S-ddddd	dddREd-S-Eddddd	dddRdd-S-dEddd	dddRdd-S-ddEdd	dddRdd-S-dddEdd	dddRdd-S-dddEdd	
	Q	dQdRdd-S-ddddd	ddQRdd-S-ddddd	dddRQd-S-ddddd	dddRQd-S-ddddd	dddRQd-S-Qddddd	dddRdd-S-dQddddd	dddRdd-S-ddQdd	dddRdd-S-dddQdd	dddRdd-S-dddQdd	
	F	dFdRdd-S-ddddd	ddFRdd-S-ddddd	dddRFd-S-ddddd	dddRFd-S-ddddd	dddRFd-S-Fddddd	dddRdd-S-dFddddd	dddRdd-S-ddFdd	dddRdd-S-dddFdd	dddRdd-S-dddFdd	
	Y	dYdRdd-S-ddddd	ddYRdd-S-ddddd	dddRYd-S-ddddd	dddRYd-S-ddddd	dddRYd-S-Yddddd	dddRdd-S-dYddddd	dddRdd-S-ddYdd	dddRdd-S-dddYdd	dddRdd-S-dddYdd	
	I	dIdRdd-S-ddddd	ddIRdd-S-ddddd	dddRIId-S-ddddd	dddRIId-S-ddddd	dddRIId-S-Iddddd	dddRdd-S-dIddddd	dddRdd-S-ddIdd	dddRdd-S-dddIdd	dddRdd-S-dddIdd	
	M	dMdRdd-S-ddddd	ddMRdd-S-ddddd	dddRMd-S-ddddd	dddRMd-S-ddddd	dddRMd-S-Mddddd	dddRdd-S-dMddddd	dddRdd-S-ddMdd	dddRdd-S-dddMdd	dddRdd-S-dddMdd	
	V	dVdRdd-S-ddddd	ddVRdd-S-ddddd	dddRVd-S-ddddd	dddRVd-S-ddddd	dddRVd-S-Vddddd	dddRdd-S-dVddddd	dddRdd-S-ddVdd	dddRdd-S-dddVdd	dddRdd-S-dddVdd	
	L	dLdRdd-S-ddddd	ddLRdd-S-ddddd	dddRLd-S-ddddd	dddRLd-S-ddddd	dddRLd-S-Lddddd	dddRdd-S-dLddddd	dddRdd-S-ddLdd	dddRdd-S-dddLdd	dddRdd-S-dddLdd	
	N	dNdRdd-S-ddddd	ddNRdd-S-ddddd	dddRNd-S-ddddd	dddRNd-S-ddddd	dddRNd-S-Nddddd	dddRdd-S-dNddddd	dddRdd-S-ddNdd	dddRdd-S-dddNdd	dddRdd-S-dddNdd	
	P	dPdRdd-S-ddddd	ddPRdd-S-ddddd	dddRPd-S-ddddd	dddRPd-S-ddddd	dddRPd-S-Pddddd	dddRdd-S-dPdnd	dddRdd-S-ddPd	dddRdd-S-dddPd	dddRdd-S-dddPd	

Fig 13. PSSM Logo from analysis of
d??R??S????d superset of peptides with AKT1

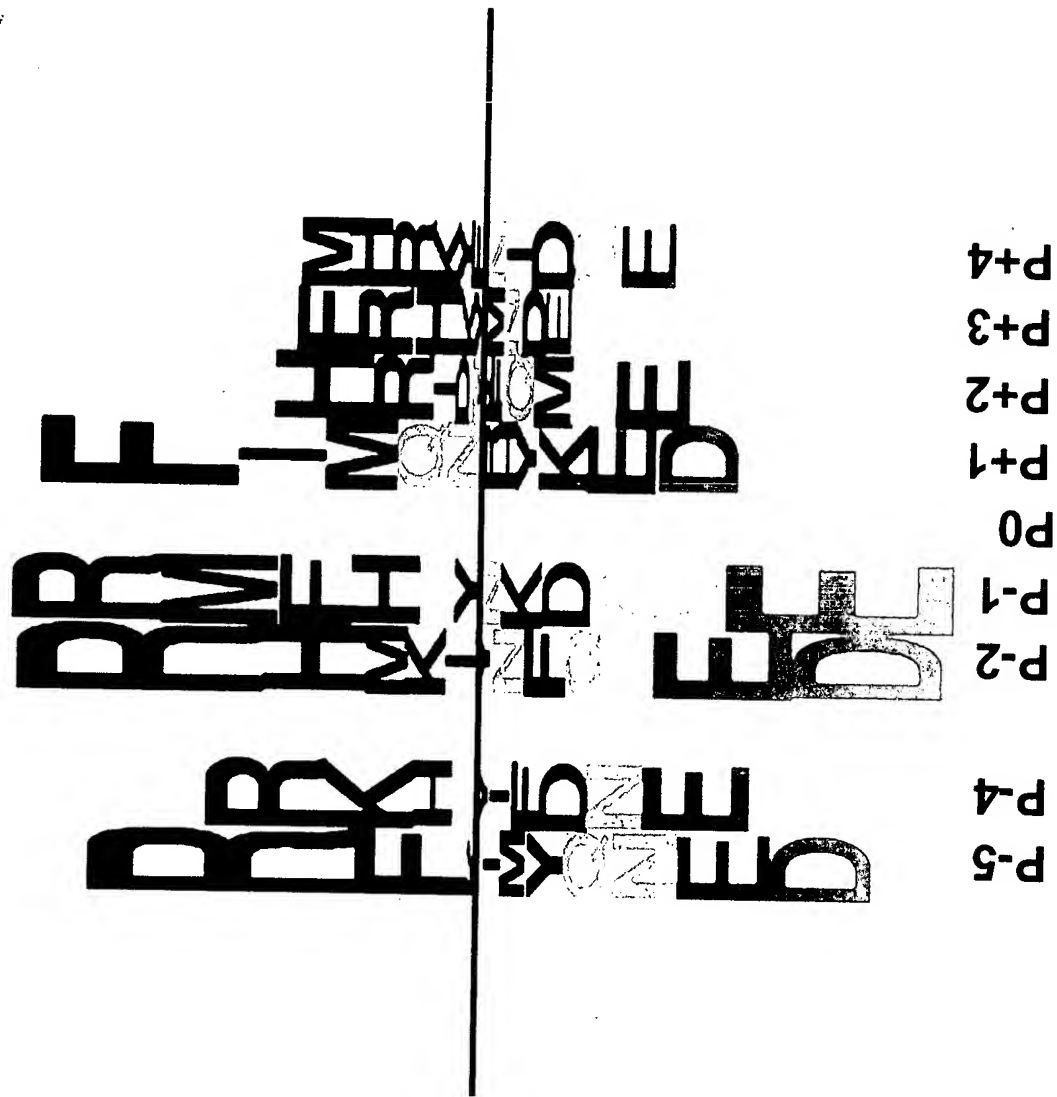


Fig 14: Issues related to abundance of residues in degenerate positions

Amino Acid		Target percentages			Estimated incorporation efficiency	Reagent parts per hundred	Percent by sequencing
		Plan 1	Plan 2	Plan 3			
Code	Name	Equal Abundance	Abundance In Human Proteome	Abundance in PKC substrates			
A	Alanine	5	7.1	6.6	1.1	8	15.8
C	Cysteine	5	2.4	0.8		0	
D	Aspartic	5	4.5	5.8	1.0	6	5.9
E	Glutamic	5	6.8	7.3	1.2	6	6.1
F	Phenylalanine	5	3.6	3.2	1.2	4	3.8
G	Glycine	5	6.9	7	1.0	8	9.2
H	Histidine	5	2.7	1.7	0.9	4	2.7
I	Isoleucine	5	4.2	3.3	0.7	4	1.6
K	Lysine	5	5.7	7.1	1.1	6	8.9
L	Leucine	5	9.8	6.8	0.9	6	9.1
M	Methionine	5	2.2	1.9	1.1	2	2.7
N	Asparagine	5	3.5	2.9	1.0	4	3.0
P	Proline	5	6.5	7.6	1.0	6	3.7
Q	Glutamine	5	4.8	2.8	1.2	6	3.9
R	Arginine	5	5.8	8.9	1.1	6	5.9
S	Serine	5	8.4	12.2	1.1	8	4.6
T	Threonine	5	5.4	5.9	0.8	6	3.1
V	Valine	5	5.9	4.3	0.8	4	3.5
W	Tryptophane	5	1.3	0.3		2	0.2
Y	Tyrosine	5	2.5	3.6	0.9	4	6.2

FIG. 15: Detection of specific phosphorylation of SHP-1 by Western blot with pPKC antibody which is augmented following stimulation by the T-cell receptor

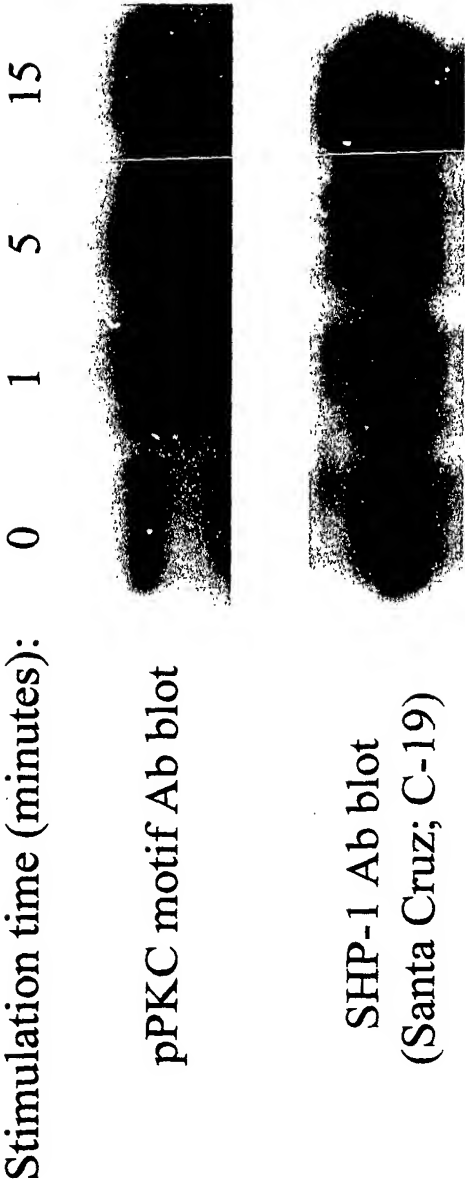


FIG. 16: Binding of pPKC antibody to phosphopeptides corresponding to those sites

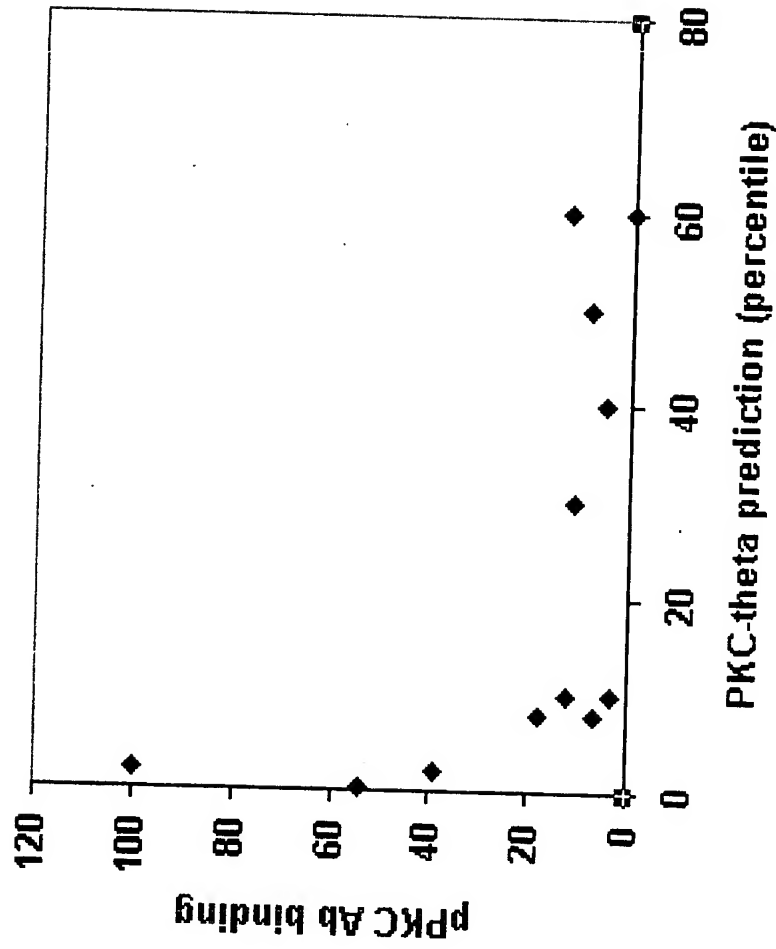


FIG. 17: Scores derived from different test sets tested at different times are reproducible and scores extrapolated for untested residues can be adequate

Residue		Test Set	
		#1	#2
Experimentally determined	D	1.3	1.3
	E		-0.9
	N	-0.9	-0.5
	C	0.0	0.5
	R		
	K		
	H	0.0	-0.2
	S	-0.2	-0.3
	T		0.2
		-0.8	-1.0
	L	0.3	0.7
	M		1.8
	F	0.5	1.4
	Y		0.5
	W	-0.3	-0.4
	G	-0.8	-0.7
	A	-0.7	-0.6

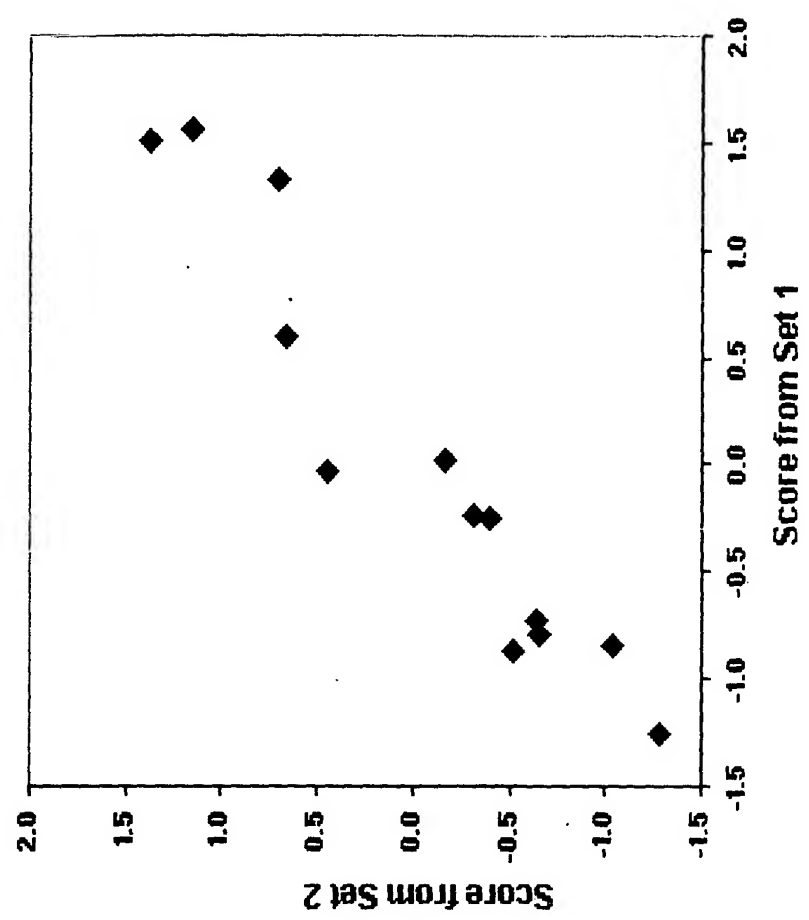


Fig 19. Distribution of PKC scores sites in proteins encoded by 15651 human genes

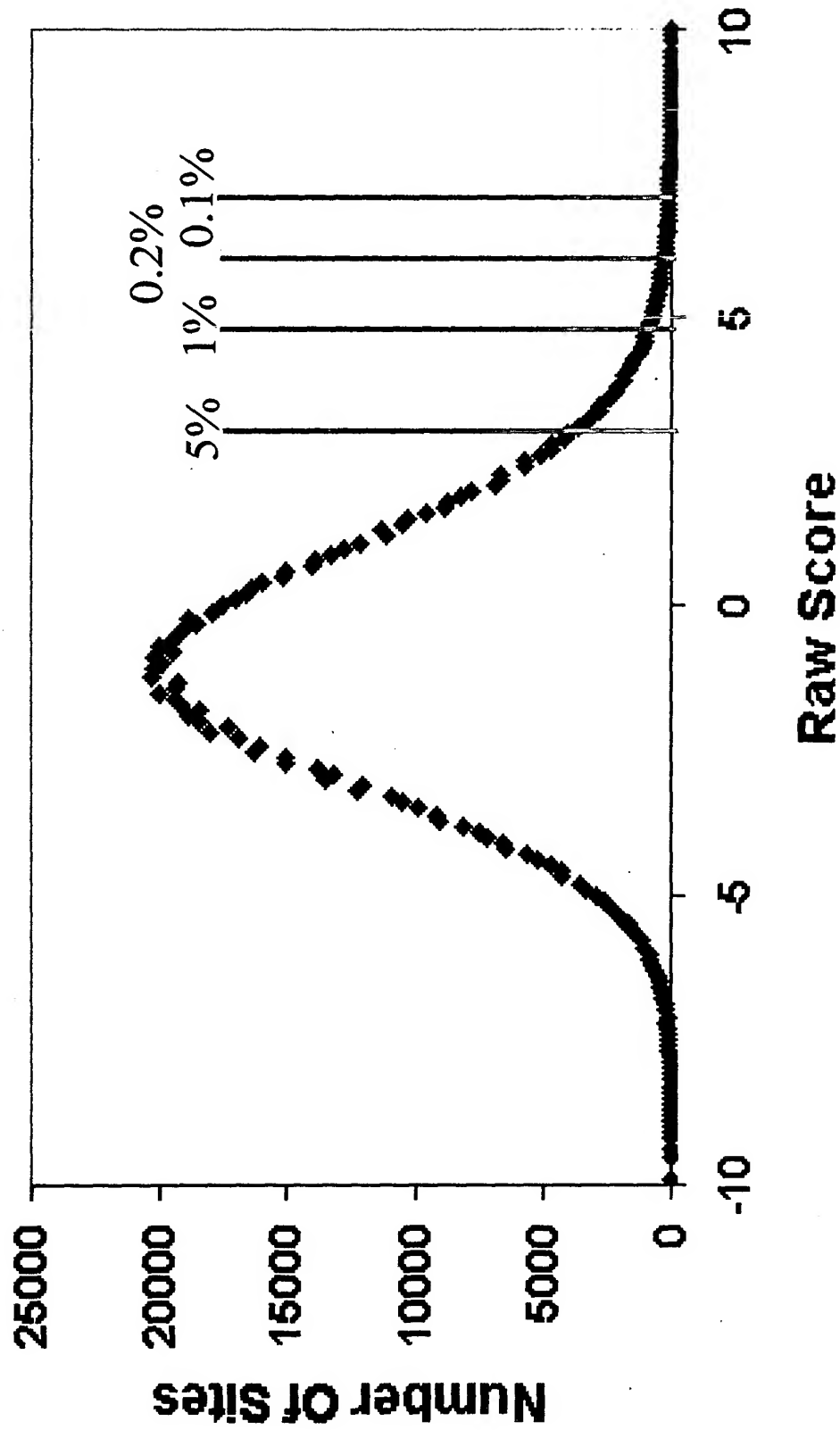
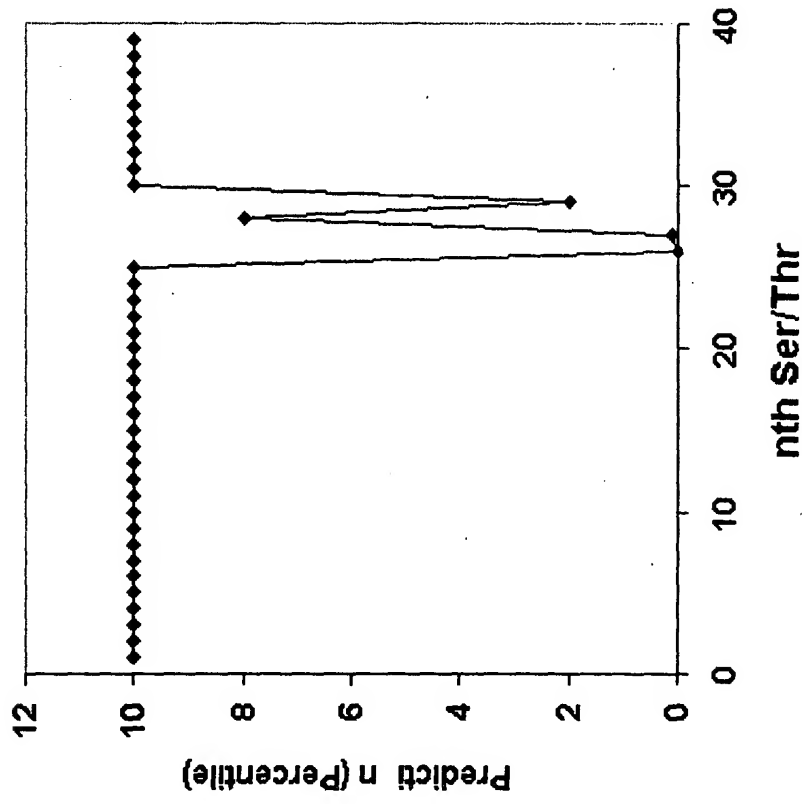


Fig 20: The PKC site prediction algorithm correctly predicts sites on MARCKS



Order	Sequence	PD Residue Number	Percentile Predictions		
			PKC Theta	AKT1	PKA
23	KAEDGATP-S-PSNETPKK	145	90	40	100
24	EDGATPSP-S-NETPKKKK	147	90	70	80
25	ATPSPSNE-T-PKKKKKKRF	150	10	80	100
26	PKKKKKRF-S-FKKSFKLS	159		0.9	10
27	KKRFSFKK-S-FKLSGFSF	163		10	10
28	SFKKSKFL-S-GFSFKKNK	167	8	70	10
29	KSFKLSGF-S-FKKNKKEA	170	2	20	90
30	AAAEAGAA-S-GEQAAAPG	211	100	40	80
31	VAPEKPPA-S-DETKAAEE	252	70	40	80

FIG. 21. High similarity in specificity between novel and classical PKC isoforms, but atypical PKC differs more and great divergence seen with AKT1 and PKA

	Correlation (arithmetic)				
	alpha	delta	epsilon	zeta	PKA
alpha		0.86	0.89	0.69	0.38
delta	0.86		0.89	0.73	0.63
epsilon	0.89	0.89		0.76	0.50
zeta	0.69	0.73	0.76		0.35
AKT1	0.38	0.63	0.50	0.35	
PKA	0.29	0.35	0.38	0.28	1.00

Fig 22. Differences between PSSM Logos of different kinases analyzed with the same peptide collections

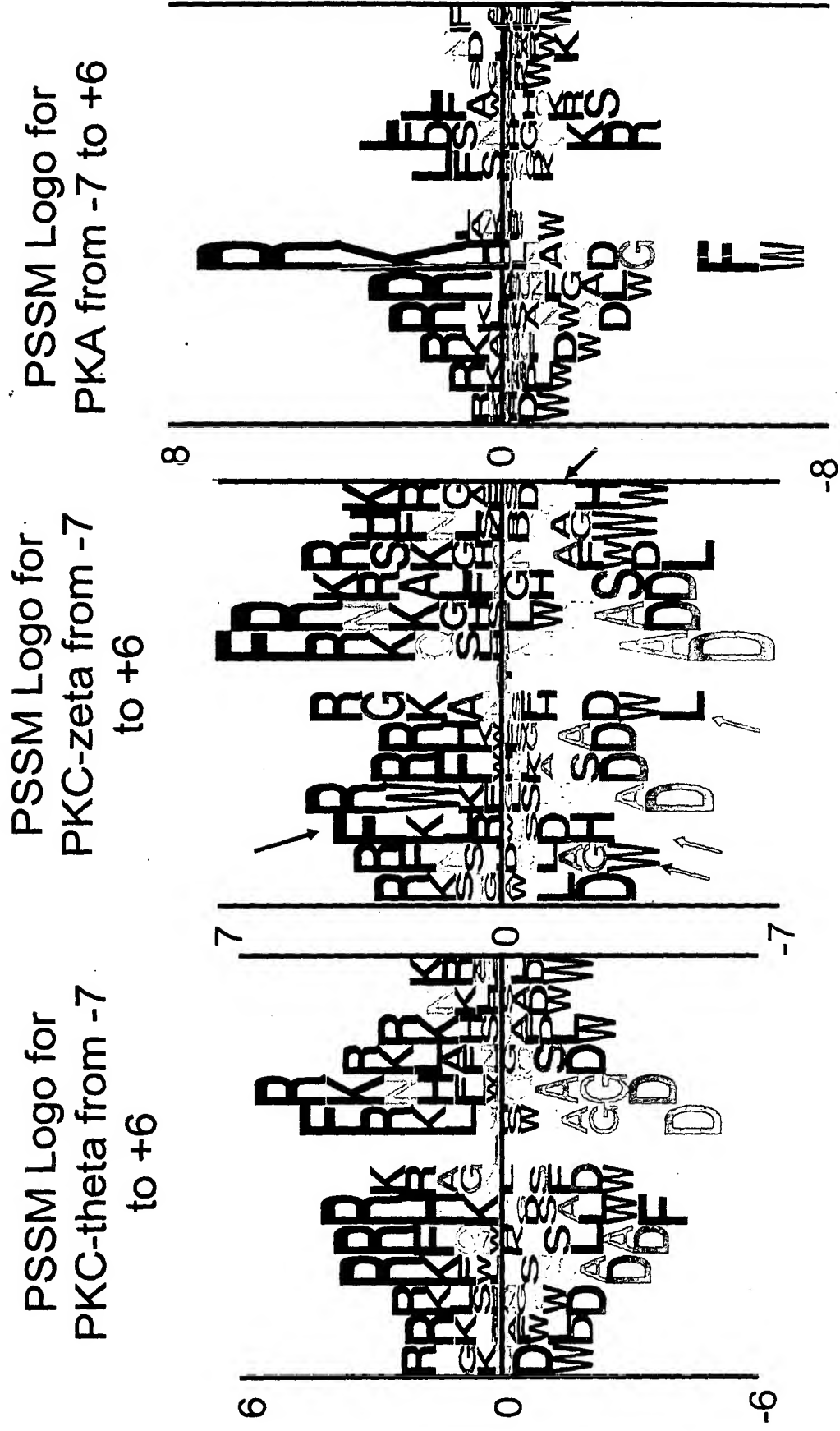


Fig 23. Prediction for PKC-zeta predicts
PKC-zeta better than PKC-delta

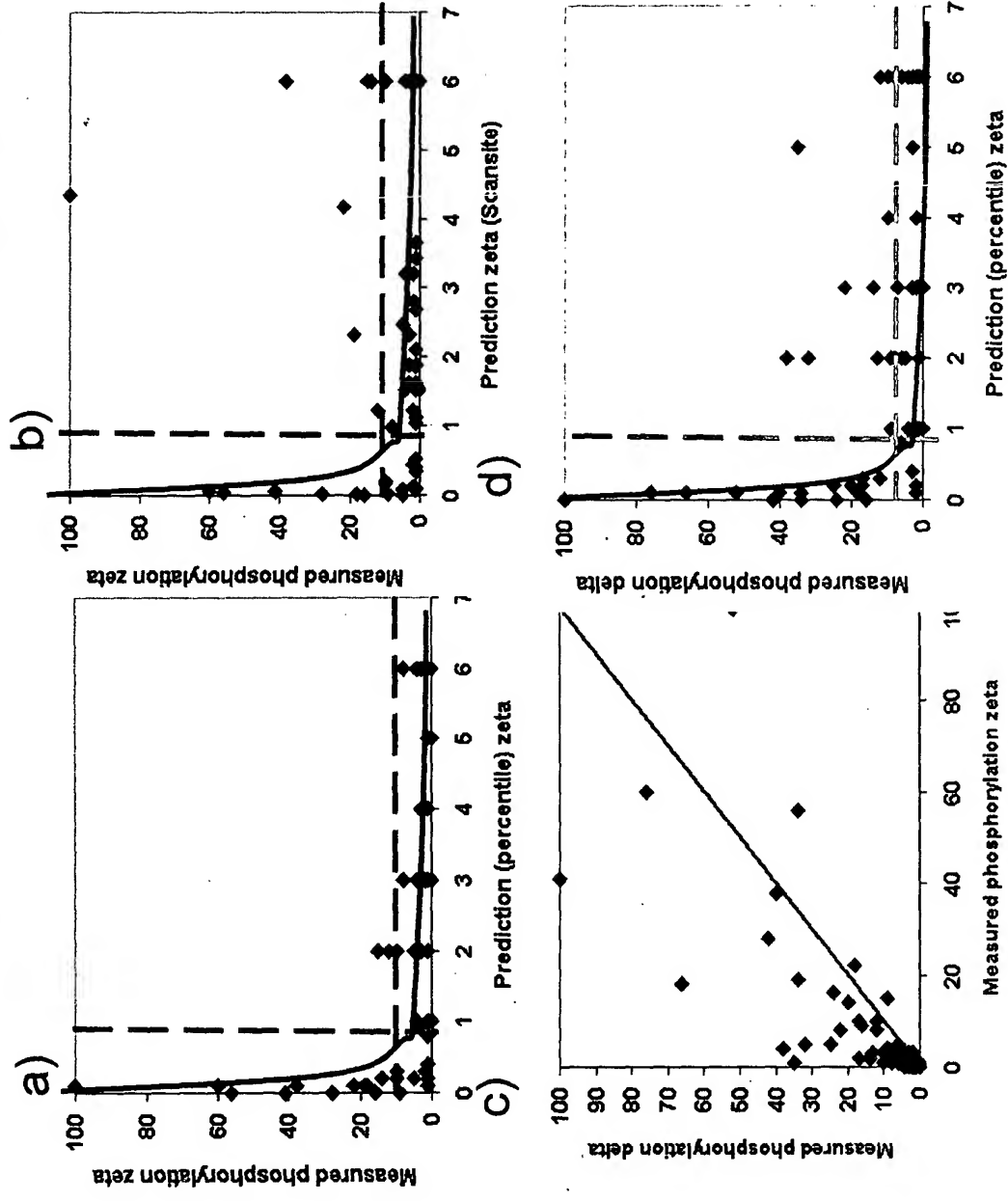


FIG. 24. Scoring changes in peptides that are less phosphorylated by PKC-zeta than PKC-delta

Peptide	Measured phosphorylation	Predicted percentile	-7	-6	-5	-4	-3	-2	-1	0	+1	+2	+3	+4	+5	+6
1	difference	34	A	A	R	K	K	R	I	S	V	K	K	K	O	E
	zeta	1	0.1	0.4	0.2	0	0	-0.1		-0.1	0.3	-0.6	-0.7	-0.1	0.5	0.1
	delta	35	-0.1	-0.6	0.7	0.8	-0.2	1.9	-1.6	0.2	0.4	1.9	1.5	1.0	-0.5	-0.5
2	difference	34	K	I		K	R	R	G	S	V	H	R	T	S	
	zeta	4	-0.2	0.1		0	-0.7	0.4	-1	-0.1	0.3	-0.3	-0.5	-0.6	0.2	
	delta	38	0.6	-0.6	-1.4	0.8	2.5	-0.6	1.5	0.2	0.4	1.1	1.3	1.0	-0.2	-0.4
3	difference	10	G	A			R	R	S	S	I	R	N	A	H	
	zeta	3	0.1	0.4		0.3	-0.7	-0.1	-0.3	-0.1	0.3	-2	0	0.2	-0.8	
	delta	13	0.3	-0.6	-1.4	-0.7	2.5	1.9	-0.1	0.2	0.4	3.6	0.3	-0.5	1.0	
4	difference	12	A	G	S	F	K	R		S	I	K	K	I	V	
	zeta	2	0.2	0.7	0.3	0.0	0.1	0.2	-0.1	-0.1	0.4	0.1	-0.3	-0.1	-0.3	
	delta	14	-0.2	-0.6	-0.5	0.4	-0.3	1.6	0.5	0.2	0.3	1.2	1.1	-1.3	0.6	
5	difference	14	W		K	G	K	R	R	S	K	A	R	K	K	R
	zeta	8	0.9	-0.4	-0.4	-0.1	0	-0.1	-0.9	-0.1	-0.3	0.6	-0.5	-0.1	0.2	-0.3
	delta	22	-1.3	0.9	-0.1	-0.2	-0.2	1.9	1.6	0.2	1.0	-1.6	1.3	1.0	0.3	1.0
6	difference	27	I	V	I	V	K	R	A	S	L	K	R	G	K	
	zeta	5	0.1	0.5	-0.3	0.3	0	-0.1	-0.7	-0.1	0.3	-0.6	-0.5	-0.6	0.2	-0.6
	delta	32	-0.1	-0.5	0.8	-0.1	-0.2	1.9	1.2	0.2	0.4	1.9	1.3	0.6	0.3	-0.9
			0.0	0.0	0.5	0.2	-0.2	1.8	0.5	0.1	0.7	1.3	0.8	0.0	0.5	-0.3

FIG. 25 Position-specific residue preference for PKA and PKG determined using the PKC superset

PKA

PKG

	'4	'3	'2	'1	P0	'+1	'+2	'+3
D	0.6	1.0	0.6	0.9		1.0		0.9
N	0.7	0.8	0.7	1.4		1.0	1.5	1.2
Q	0.7	0.8	0.6	1.0		0.9	0.6	0.8
R				1.1		1.2	0.5	0.7
K	1.3	1.1		1.1		1.0	0.5	0.8
H	1.1	0.9		0.9		1.1	0.8	0.8
S	0.8	1.1	0.9	0.9	0.9	1.0		0.6
P	1.3	1.2	0.5	0.8		0.3	1.1	0.9
L	1.2	0.6	0.7	1.3				
F	1.1	0.7	0.3	1.0				
W	0.7	0.6	0.3	0.6		1.2	1.0	1.2
G	0.9	0.7	0.9	1.0		0.9	0.7	1.0
A	0.8	0.7	0.6	1.2		0.9	1.0	1.6
T					1.1			

'4	'3	'2	'1	P0	'+1	'+2	'+3
0.4	1.1	0.6	0.4		0.7		0.9
0.4	1.3	0.5			0.8	1.4	1.2
0.6	1.0	0.9	1.2		0.7	0.3	0.8
						0.4	0.9
						0.4	0.8
1.3	1.0	0.6	1.5		0.7	1.2	0.2
0.6	0.9	1.0	0.8	0.9	0.8		0.7
1.0	0.9	0.6	0.5		0.5	0.5	0.9
1.1	0.6	0.5	1.2				
1.1	0.9	0.4			1.5		
0.6	0.5	0.5	0.7		1.3	1.2	
1.5	0.4	0.6	0.3		0.4	0.7	1.1
1.0	0.6	0.4	0.8		1.1	1.5	0.6
				1.1			

Fig 26. Use of peptides to analyze mutant constructs and altered conditions for kinase assay

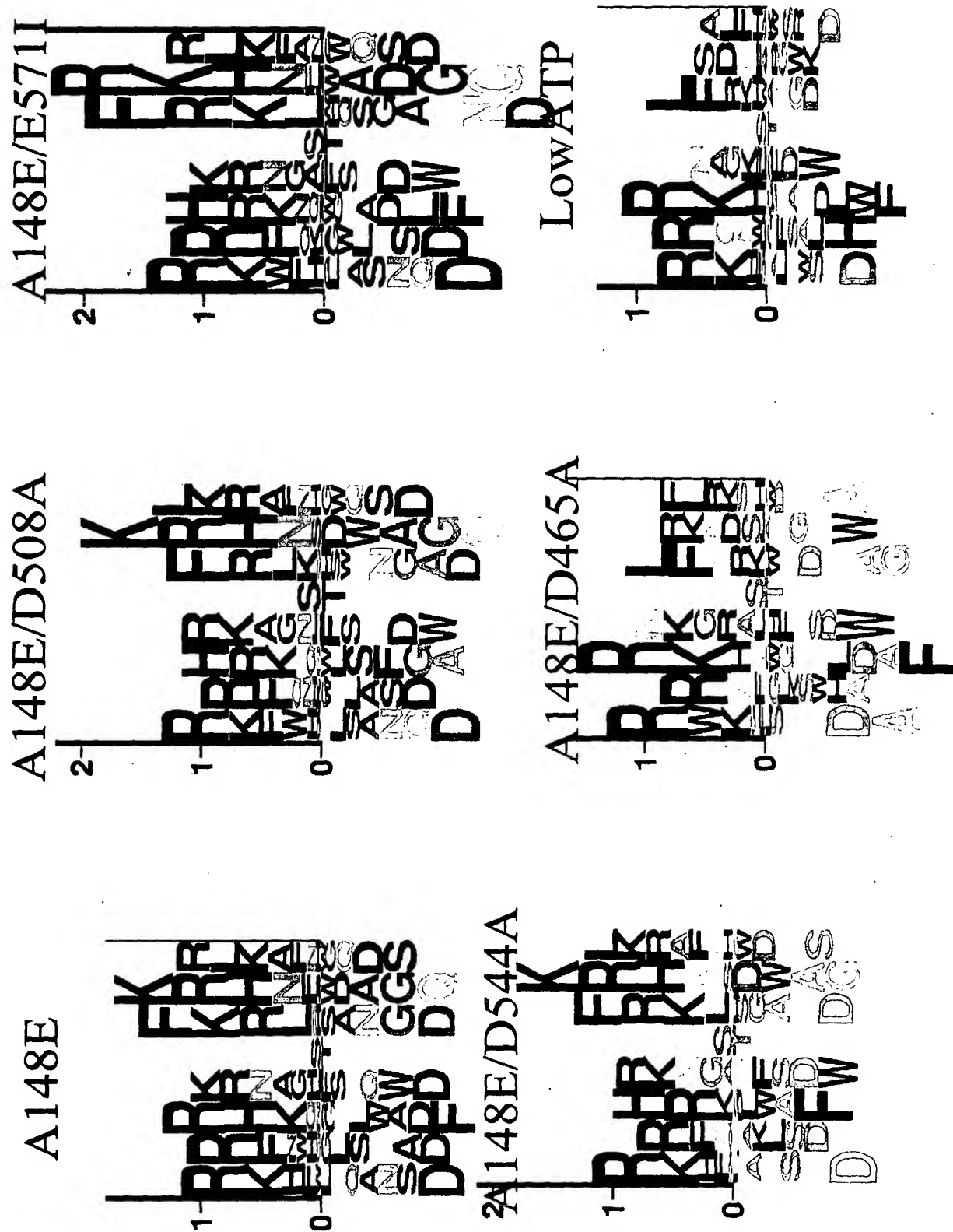


Fig 27. Details of changes observed with mutant constructs and altered conditions for kinase assay

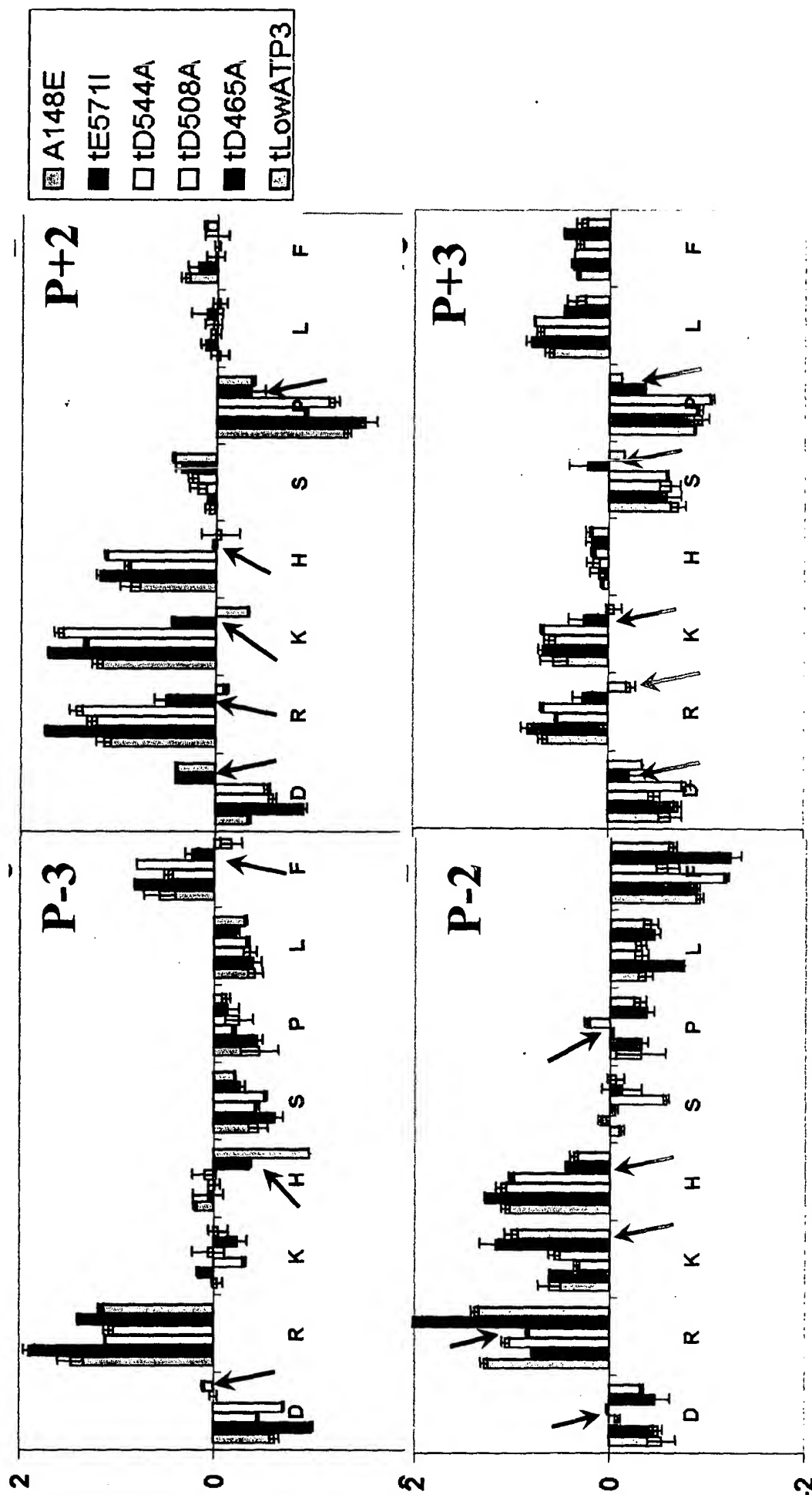


FIG. 28 details of residue references for PKC-theta
depend on anchor and phosphorylation residues

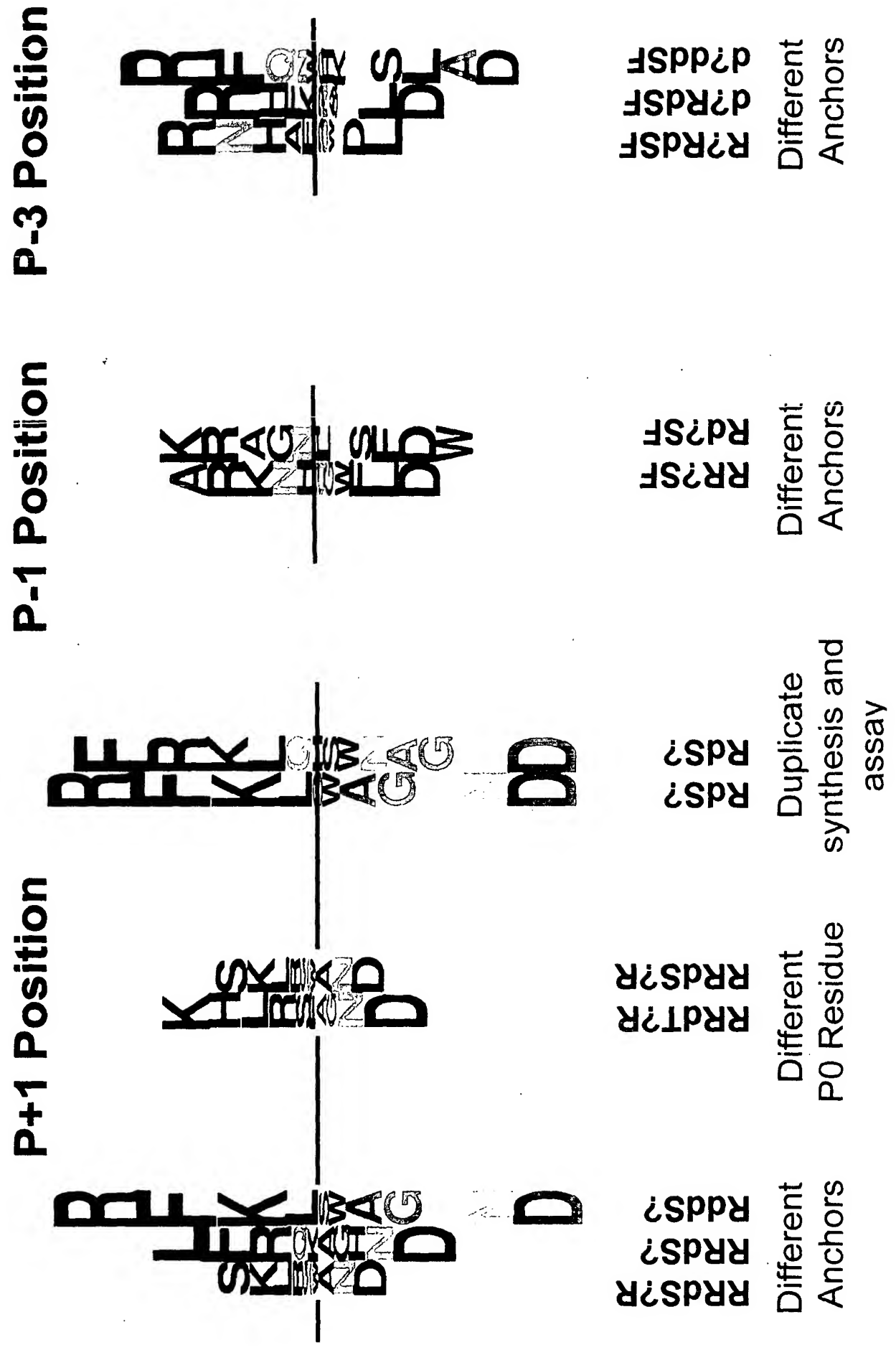


FIG. 29 Results for ROK-alpha with test sets based on ??R??T?? with only 4 query residues

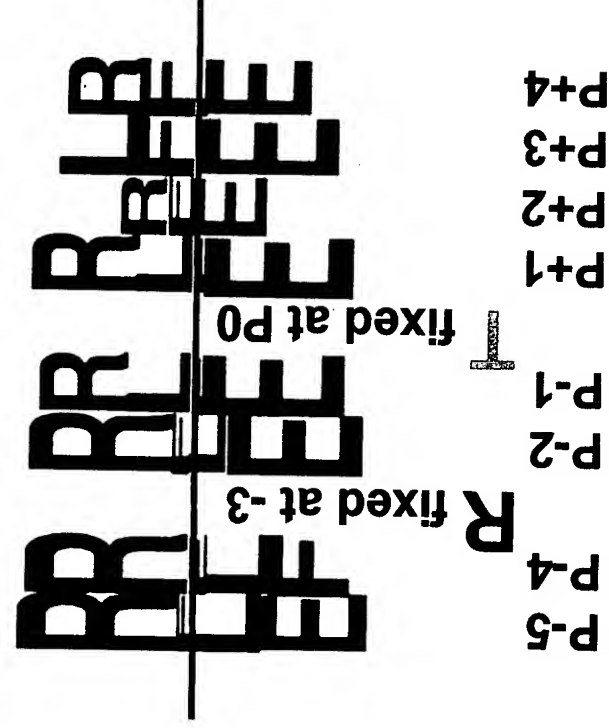


FIG. 30. Details of the R-Pair Anchor optimization set

		Position of 2nd R				
		-6	-5	-4	-3	-2
Position of 1st R	-7	RRdddddSddd	RdRdddddSddd	RddRdddddSddd	RddRdddddSddd	RdddddRdSddd
	-6		dRRdddddSddd	dRdRdddddSddd	dRddRdddddSddd	dRdddddRdSddd
	-5			ddRRdddddSddd	ddRdRdddddSddd	ddRdddddRdSddd
	-4				dddRRdddddSddd	dddRdRdSddd
	-3					dddddRRdSddd

		Position of 2nd R		
		-1	+1	+2
Position of 1st R	-7	RdddddRSddd	RdddddSRddd	RdddddSdRd
	-6	dRdddddRSddd	dRdddddSRddd	dRdddddSdRd
	-5	ddRdddddRSddd	ddRdddddSRddd	ddRdddddSdRd
	-4	dddRdddddRSddd	dddRdddddSRddd	dddRdddddSdRd
	-3	ddddRdddddRSddd	ddddRdddddSRddd	ddddRdddddSdRd
	-2	dddddRRSddd	dddddRdSRddd	dddddRdSdRd
	-1		dddddRRSRddd	dddddRRSdRd
	+1			dddddRRSRd
	+2			dddddRRSR

FIG. 31: R-Pair set results for PKA

		Position of 2nd R										
		7	6	5	4	3	2	1	+1	+2	+3	
Position of 1st R	7			0.3	-0.3			-0.8	-0.8	-0.4	-1.4	
	6				0.4			-0.5	0.1	-1.6	-0.7	
	5							-0.4	-0.8	0.4	-0.9	
	4	0.3						-0.5	-0.5	-1.9	-1.0	
	3											
	2											
	1											
	+1	-0.8	-0.5	-0.4	-0.5			-0.2	0.3	-0.1		
	+2	-0.8	0.1	-0.8	-0.5		-0.2	1.0		-0.2	-1.9	
	+3	-0.4	-1.6	0.4	-0.9		0.3	-1.4	-0.2		-2.8	
	avg	-1.4	-0.7	-0.9	-1.0		-0.1	-1.5	-1.9	-2.8		
		0.0	0.2	0.3	0.1			-0.2	-0.3	-0.5	-1.1	

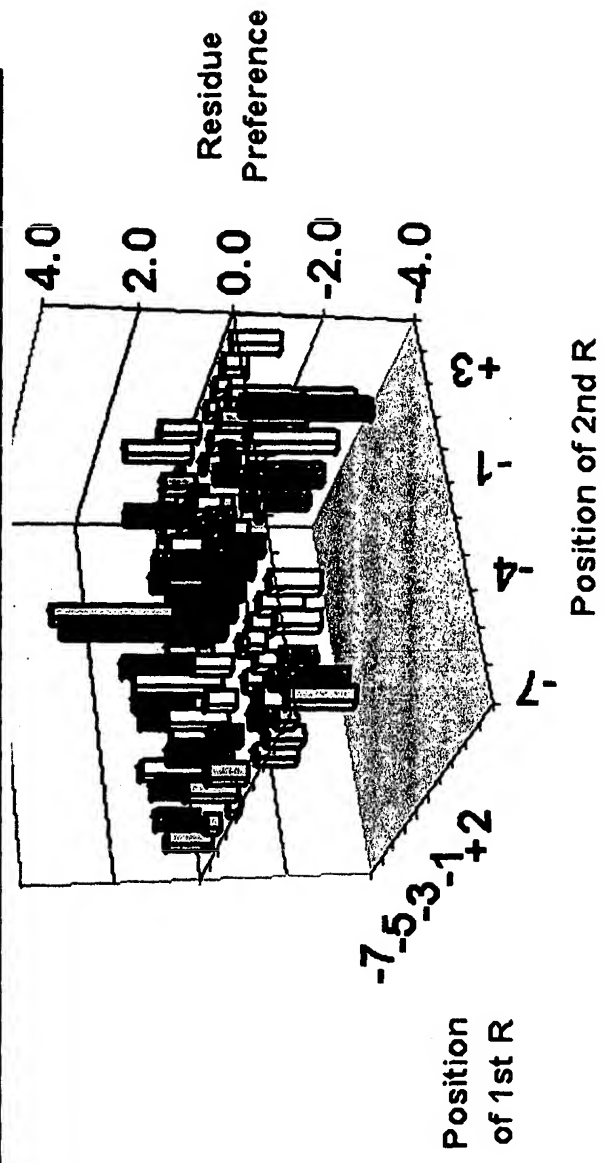


FIG. 32: R-Pair set reveals positions associated with the high preference for R

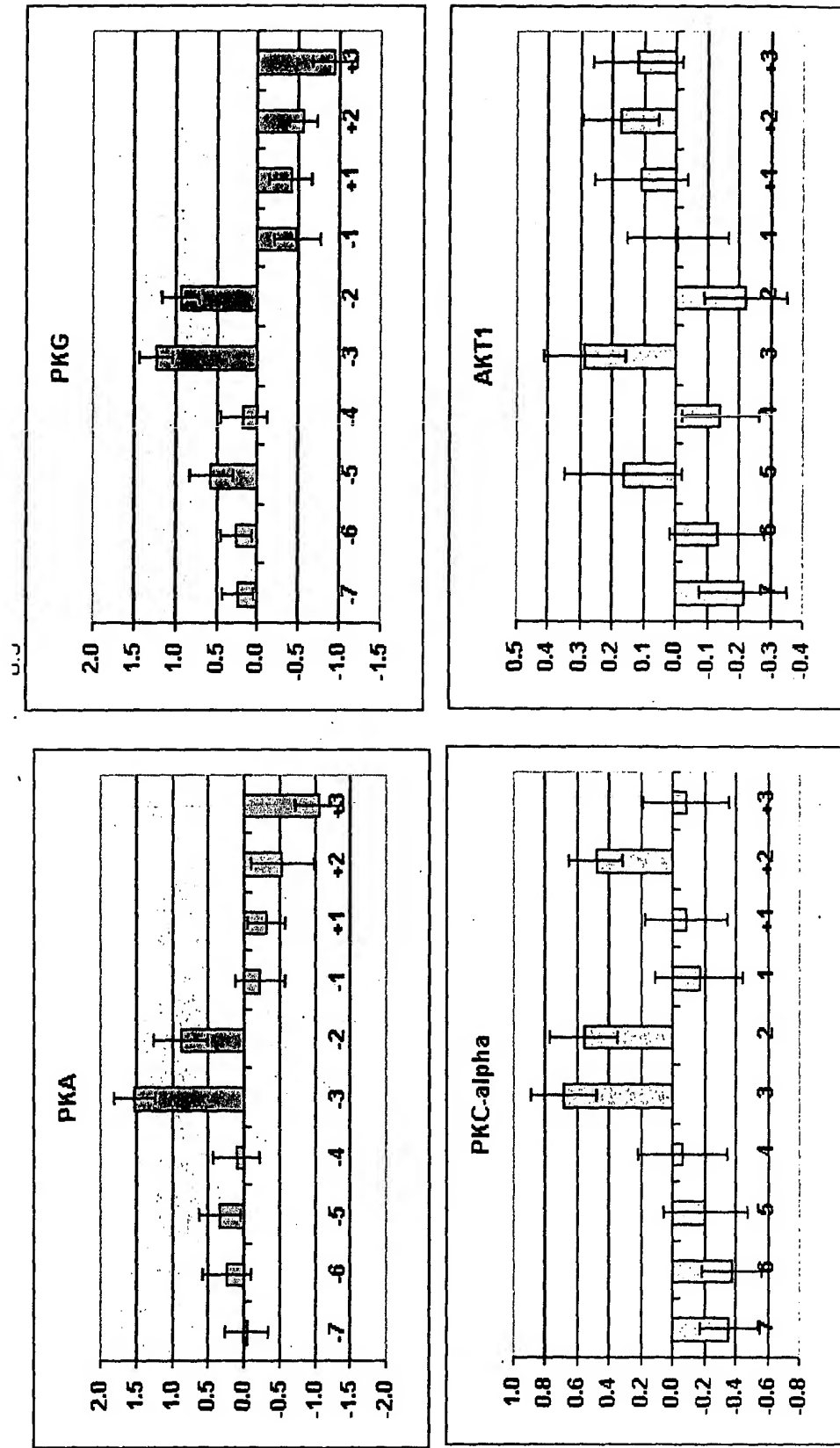


FIG. 33 : Detection of specific phosphorylation of LIMK-2 by Western blot with the pPKC antibody which is augmented following stimulation by the T-cell receptor

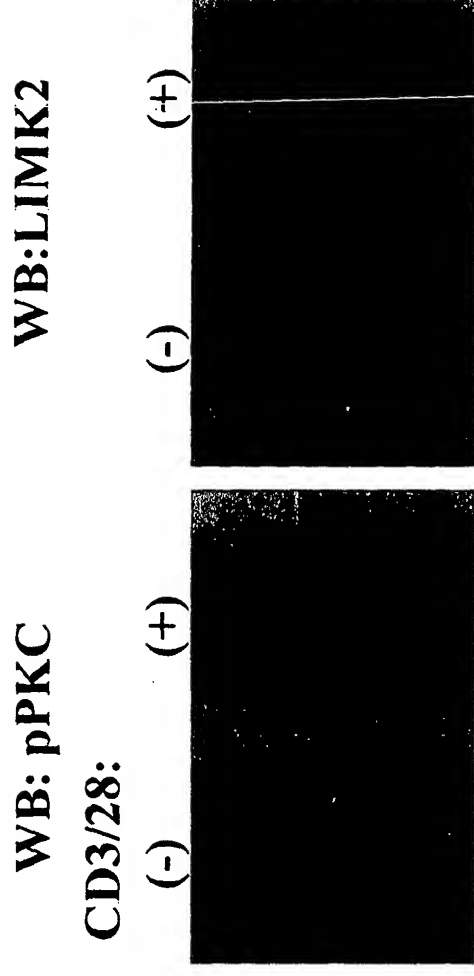


FIG. 34 : Detection of phosphorylation of MLK3 by Western blot with pPKC antibody

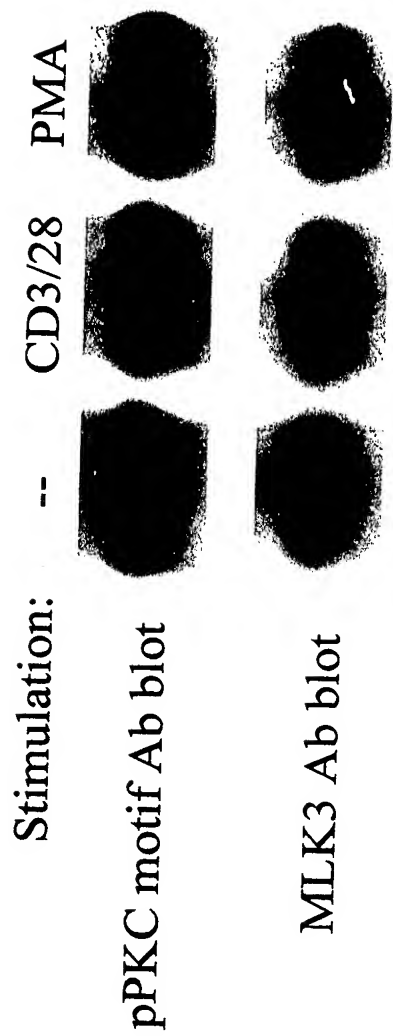


FIG. 35 Diagram of a computerized system in conjunction with which embodiments of the invention may be implemented

